

Re-run



1635

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/964,678A

DATE: 03/25/2002
TIME: 13:48:35

Input Set : N:\paola\US09964678A.RAW
Output Set: N:\CRF3\03222002\I964678A.raw

1 <110> APPLICANT: de la Monte, Suzanne
2 Wands, Jack R.
3 <120> TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs
4 Effective for the Treatment or Prevention of
5 Alzheimer's Disease
6 <130> FILE REFERENCE: 0609.4370002
C--> 7 <140> CURRENT APPLICATION NUMBER: US/09/964,678A
8 <141> CURRENT FILING DATE: 2001-09-28
9 <150> PRIOR APPLICATION NUMBER: 09/380,203
10 <151> PRIOR FILING DATE: 2000-04-25
11 <150> PRIOR APPLICATION NUMBER: PCT/US98/03685
12 <151> PRIOR FILING DATE: 1998-02-26
13 <150> PRIOR APPLICATION NUMBER: 60/038,908
14 <151> PRIOR FILING DATE: 1997-02-26
15 <160> NUMBER OF SEQ ID NOS: 14
16 <170> SOFTWARE: PatentIn version 3.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1442
20 <212> TYPE: DNA
21 <213> ORGANISM: Unknown
22 <220> FEATURE:
23 <223> OTHER INFORMATION: AD7c-NTP cDNA
W--> 24 <221> NAME/KEY: CDS
25 <222> LOCATION: (15)..(1139)
26 <223> OTHER INFORMATION:

ENTERED

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31 aat ggc gca atc tca gct cac cgc aac ctc cgc ctc ccg ggt tca agc 98
32 Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser
33 15 20 25
34 gat tct cct gcc tca gcc tcc cca gta gct ggg att aca ggc atg tgc 146
35 Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys
36 30 35 40
37 acc cac gct cgg cta att ttg tat ttt ttt tta gta gag atg gag ttt 194
38 Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe
39 45 50 55 60
40 ctc cat gtt ggt cag gct ggt ctc gaa ctc ccg acc tca gat gat ccc 242
41 Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro
42 65 70 75
43 tcc gtc tcg gcc tcc caa agt gct aga tac agg act ggc cac cat gcc 290
44 Ser Val Ser Ala Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala

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45		80		85		90		338
46	cgg	ctc	tgc	ctg	gct	aat	ttt	tgt
47	Arg	Leu	Cys	Leu	Ala	Asn	Phe	Cys
48								100
49	tgc	cca	agc	tgg	tct	cct	gag	ctc
50	Cys	Pro	Ser	Trp	Ser	Pro	Glu	Leu
51								110
52	cca	aag	tgc	tgg	gat	tac	agg	cgt
53	Pro	Lys	Cys	Trp	Asp	Tyr	Arg	Arg
54								125
55	tta	ttt	ttt	tta	aga	cac	agg	tgt
56	Leu	Phe	Phe	Leu	Arg	His	Arg	Cys
57								145
58	cag	tgg	tgt	gat	cac	agc	tca	ctg
59	Gln	Trp	Cys	Asp	His	Ser	Ser	Leu
60								160
61	cat	cct	cct	gcc	tca	gcc	tcc	caa
62	His	Pro	Pro	Ala	Ser	Ala	Ser	Gln
63								175
64	cac	tac	acc	tgg	cta	att	ttt	att
65	His	Tyr	Thr	Trp	Leu	Ile	Phe	Ile
66								190
67	agt	ctc	aac	tct	gtc	acc	cag	gct
68	Ser	Leu	Asn	Ser	Val	Thr	Gln	Ala
69								205
70	tca	ctg	caa	cct	ctg	cct	ccc	ggg
71	Ser	Leu	Gln	Pro	Leu	Pro	Pro	Gly
72								225
73	ctc	ctg	agt	agc	tgg	gac	tac	agg
74	Leu	Leu	Ser	Ser	Trp	Asp	Tyr	Arg
75								240
76	ttt	gta	ttt	tta	gta	gag	atg	ggg
77	Phe	Val	Phe	Leu	Val	Glu	Met	Gly
78								255
79	ttg	atc	tct	gga	cct	tgt	gat	ctg
80	Leu	Ile	Ser	Gly	Pro	Cys	Asp	Leu
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82	ggg	att	aca	ggc	gtg	agc	cac	cac
83	Gly	Ile	Thr	Gly	Val	Ser	His	His
84								285
85	ttg	ttt	gaa	atg	gaa	tct	cac	tct
86	Leu	Phe	Glu	Met	Glu	Ser	His	Ser
87								305
88	cca	aat	ctc	ggc	tca	ctg	caa	cct
89	Pro	Asn	Leu	Gly	Ser	Leu	Gln	Pro
90								320
91	tcc	tgt	ctc	agc	ctc	cca	agc	agc
92	Ser	Cys	Leu	Ser	Leu	Pro	Ser	Ser
93								335

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95      His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr
96      350                               355                               360
97      ttg tca ggc tgg tct caa act cct gac ctc agg tgaccacact gcctcagcct      1159
98      Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg
99      365                               370                               375
100     tccaaagtgc tgggattaca ggcgtgagcc acctcaccga gccgggctaatt ttagataaaa      1219
101     aaatatgtag caatgggggg tcttgctatg ttgccaggc tgggtctcaaa cttctggctt      1279
102     catgcaatcc ttccaaatga gccacaacac ccagccagtc acatttttta aacagttaca      1339
103     tctttatttt agtatactag aaagtaatac aataaacatg tcaaacctgc aaattcagta      1399
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109 <213> ORGANISM: Unknown
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116     20                               25                               30
117     Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg
118     35                               40                               45
119     Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly
120     50                               55                               60
121     Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala
122     65                               70                               75                               80
123     Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu
124     85                               90                               95
125     Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp
126     100                              105                              110
127     Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp
128     115                              120                              125
129     Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu
130     130                              135                              140
131     Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp
132     145                              150                              155                              160
133     His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala
134     165                              170                              175
135     Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp
136     180                              185                              190
137     Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser
138     195                              200                              205
139     Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro
140     210                              215                              220
141     Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser
142     225                              230                              235                              240
143     Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu

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146				260				265	
147	Pro	Cys	Asp	Leu	Pro	Ala	Ser	Ala	Ser
148				275				280	
149	Val	Ser	His	His	Ala	Arg	Leu	Ile	Phe
150				290				295	
151	Glu	Ser	His	Ser	Val	Thr	Gln	Ala	Gly
152				305				310	
153	Ser	Leu	Gln	Pro	Leu	Pro	Pro	Gly	Leu
154				325				330	
155	Leu	Pro	Ser	Ser	Trp	Asp	Tyr	Gly	His
156				340				345	
157	Phe	Cys	Ile	Phe	Ile	Arg	Gly	Gly	Val
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171	agtagctggg	attacaggca	tgtgcaccac	gctcggctaa	ttttgtattt	tttttagta	180		
172	gagatggagt	ttactccat	gttggtcagg	ctggctcga	actcccgacc	tcagatgatc	240		
173	tcccgtctcg	gcctgcccac	agtgtcgaga	ttacaggcat	gagccacat	gcccggcctc	300		
174	tgcctggcta	atttttgttg	tagaaacagg	gtttcactga	tggtgcccac	gctggtctcc	360		
175	tgagctcaag	cagtcacact	gcctcagcct	cccaaagtgc	tgggattaca	ggcgctcagcc	420		
176	gtgcctggcc	tttttatatt	atttttttta	agacacaggt	gtaccactct	taccaggat	480		
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181	ccagcctcct	gagtagctgg	gactacaggc	gcccaccacg	cctagctaatt	ttttttgtat	780		
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185	aatggcaaat	ctcggctact	cgcaacctct	gcctcccggg	tcaagcgatt	ctcctgtctc	1020		
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189	ggctaatttg	gaataaaaaa	tatgtagcaa	tgggggctctg	ctatgttgcc	caggctgggc	1260		
190	tcaaacttct	ggcttcagtc	aatccttcca	aatgagccac	aacacccagc	cagtcacatt	1320		
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192	c						1381		
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Input Set : N:\paola\US09964678A.RAW
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195 <211> LENGTH: 1418
196 <212> TYPE: DNA
197 <213> ORGANISM: Unknown
198 <220> FEATURE:
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203      agtaggctgg gattacaggc atgtgcacca cgctcggcta attttgtatt tttttttagt      180
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206      ggctaatttt tgtggtagaa acagggtttc actgatgtgc ccaagctggt ctcctgagct      360
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208      tggccttttt attttatttt ttttaagaca cagggtgtccc actcttacct aggatgaagt      480
209      gcagtgggtg gatcacagct cactgcagcc ttcaactctg agatcaagca tcctcctgcc      540
210      tcagcctccc aaagtagctg ggaccaaaga catgcaccac tacacctggc taatttttat      600
211      ttttattttt aattttttga gacagagtct caactctgtc acccaggctg gagtgcagtg      660
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217      atggccaaat ctcggtcac tgcaacctct gcctcccggg ctcaagcgat tctcctgtct      1020
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219      ttcattagag gcggggtttc accatatttg tcaggctggt ctcaaactcc tgacctcagg      1140
220      tgaccacact gcctcagcct tccaaagtgc tgggattaca ggcgtgacgc ctcaccagc      1200
221      cggctaattt agataaaaaa atatgtagca atgggggggtc ttgctatgtt gccaggctg      1260
222      gtctcaaaact tctggcttca tgcaatcctt ccaaagagc cacaacaccc agccagtcac      1320
223      atttttaaac agttacatct ttatttttagt atactagaaa gtgatacgat aacatggcgg      1380
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227 <211> LENGTH: 22
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229 <213> ORGANISM: Artificial Sequence
230 <220> FEATURE:
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236 <211> LENGTH: 24
237 <212> TYPE: DNA
238 <213> ORGANISM: Artificial Sequence
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246 <212> TYPE: DNA

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:12; N Pos. 11
Seq#:13; N Pos. 11
Seq#:14; N Pos. 11

VERIFICATION SUMMARY

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L:7 M:270 C: Current Application Number differs, Wrong Format
L:24 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:27 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:295 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:298 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:12
L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:307 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:310 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:13
L:311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:319 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:322 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:14
L:323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0